Figure S1

A

Macrophages, before batch adjustment

PC2: 14.61% variance

PC1: 35.26% variance

Legend:
- uninf4
- uninf24
- uninf48
- uninf72
- infLM4
- infLM24
- infLM48
- infLM72
- infLA4
- infLA24
- infLA48
- infLA72
- beads4
- beads24
- beads48
- beads72

B

Macrophages, after batch adjustment

PC2: 18.40% variance

PC1: 40.95% variance

Legend:
- uninf4
- uninf24
- uninf48
- uninf72
- infLM4
- infLM24
- infLM48
- infLM72
- infLA4
- infLA24
- infLA48
- infLA72
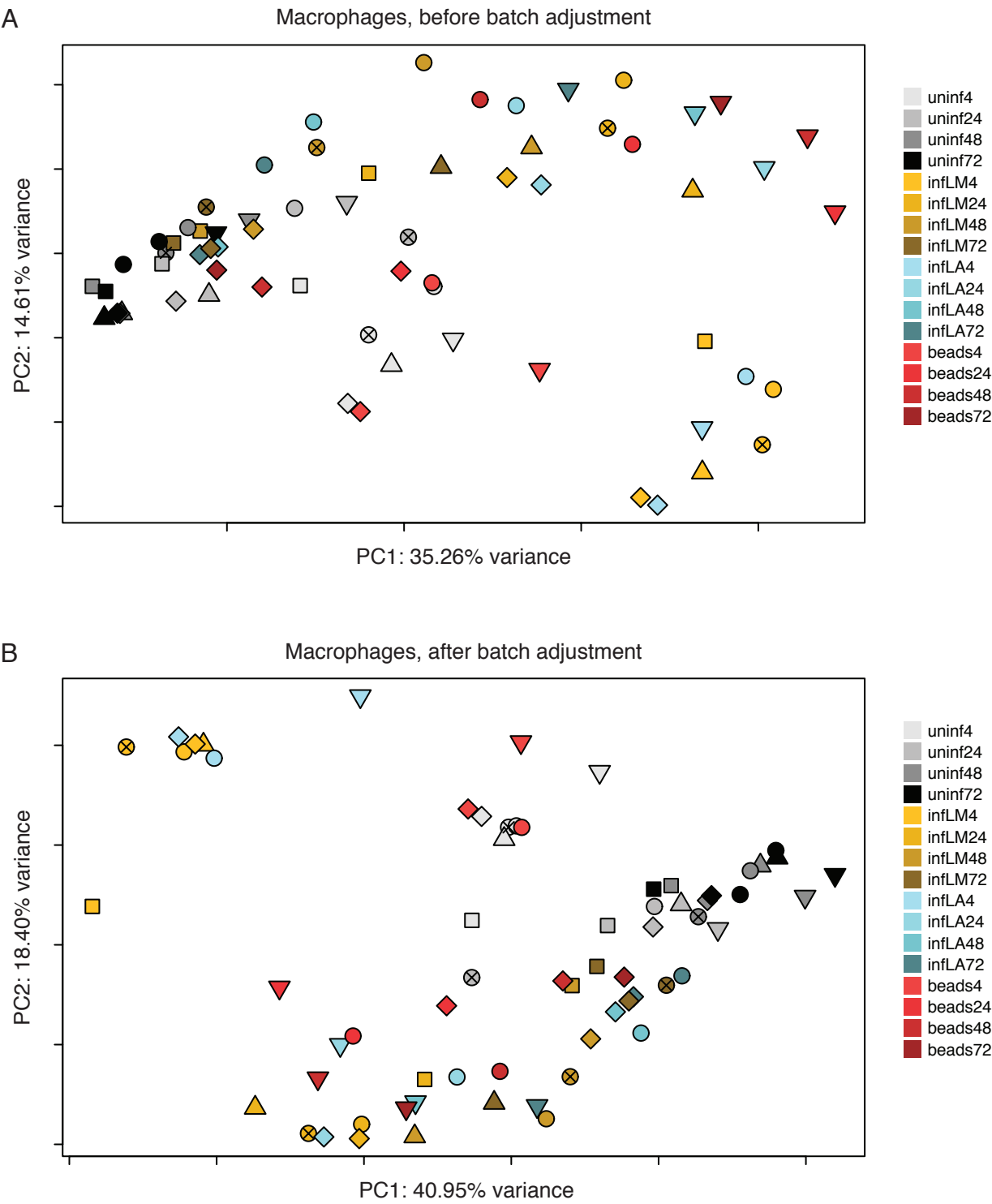- beads4
- beads24
- beads48
- beads72

Figure S1. Global gene expression profiles of *Leishmania*-infected and bead-containing macrophages before and after batch adjustment. RNA-seq was carried out on human macrophages infected with *L. major* or *L. amazonensis* at 4, 24, 48, and 72 hpi as well as on macrophages that had ingested latex beads and uninfected controls. Principal component analysis (PCA) plots are shown for all human macrophage samples both before (**A**) and after (**B**) including experimental batch as a covariate in the statistical model. The first two principal components are shown on the X and Y axes, respectively, with the proportion of total variance explained by the PC indicated. Each experimental sample is represented as a single point with color hue indicating sample type (yellow for *L. major*-infected cells, blue for *L. amazonensis*-infected cells, red for bead-containing cells, and gray for uninfected cells), color shade indicating time point (light to dark representing 4 to 72 hpi), and shape indicating experimental batch. Samples are named according to sample type ("infLM" for *L. major*-infected cells, "infLA" for *L. amazonensis*-infected cells, "beads" for bead-containing cells, and "uninf" for uninfected cells) and time point (4, 24, 48, or 72 hpi). All analyses were performed after filtering out non- and lowly-expressed genes and quantile normalization.